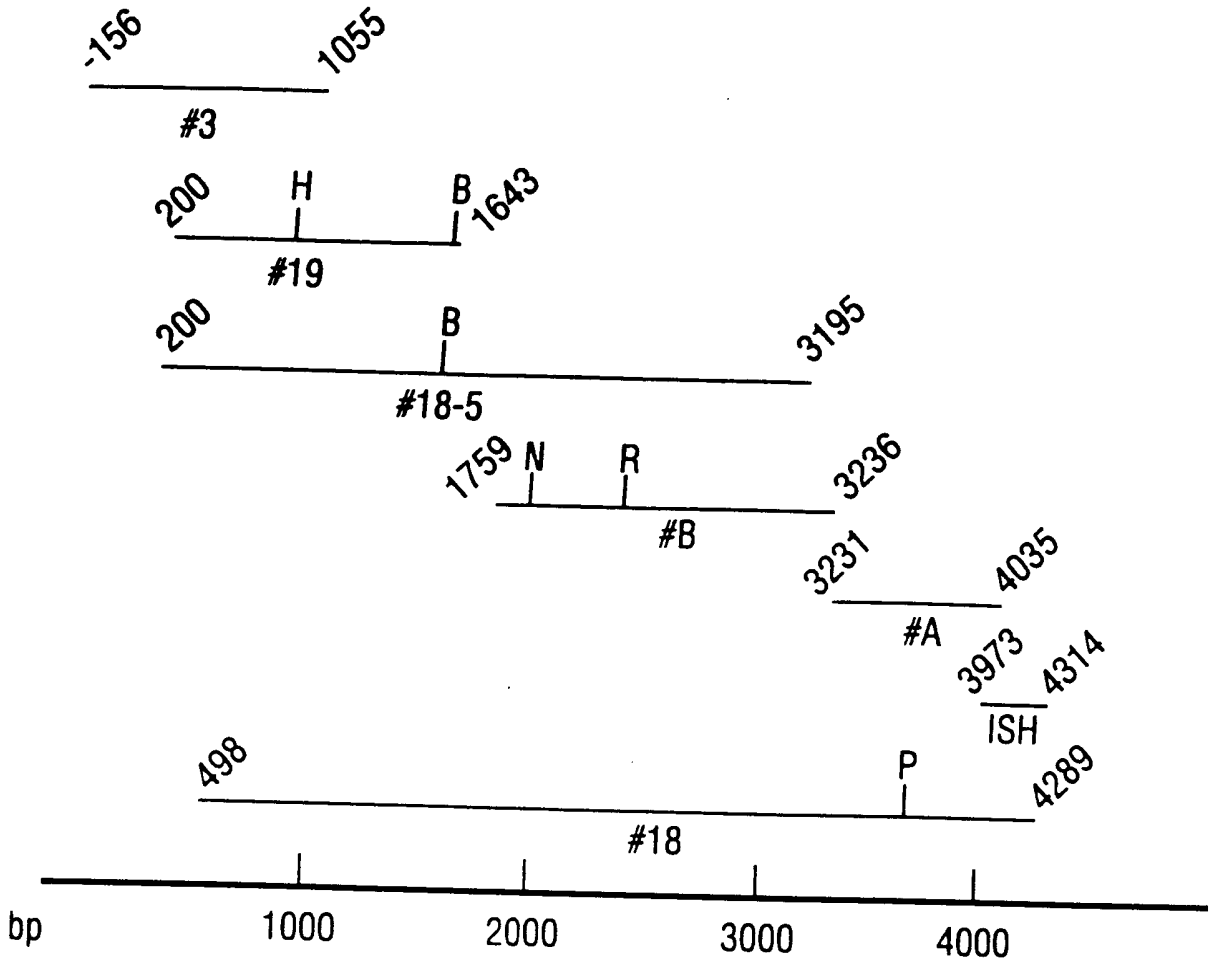


FIG. 1

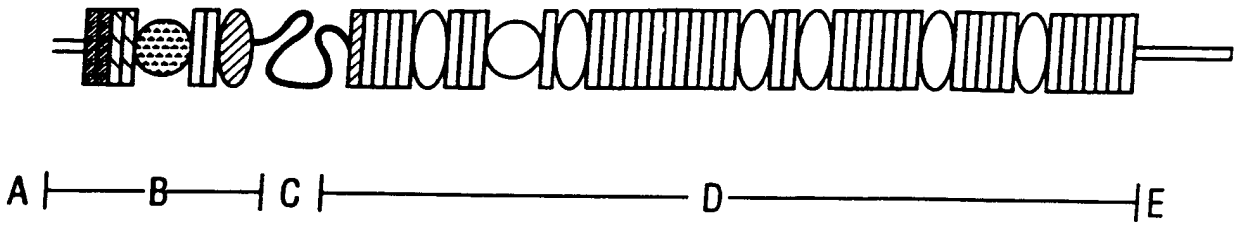


FIG. 2A

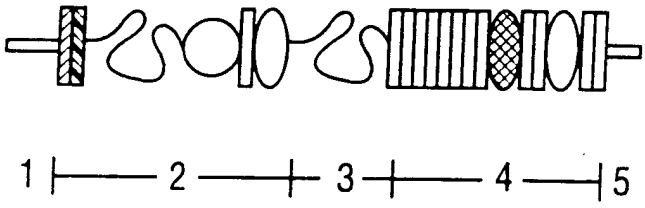


FIG. 2B

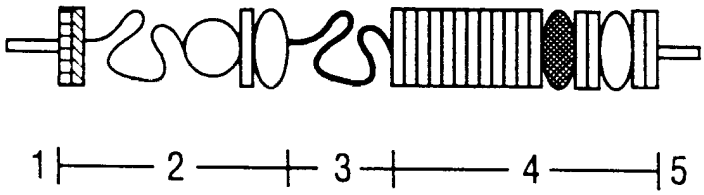
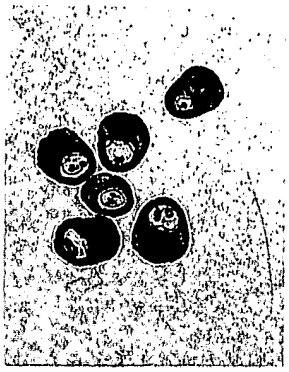
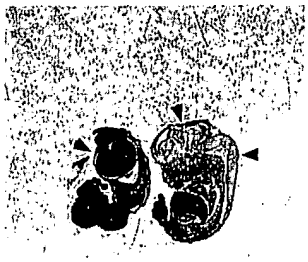


FIG. 2C

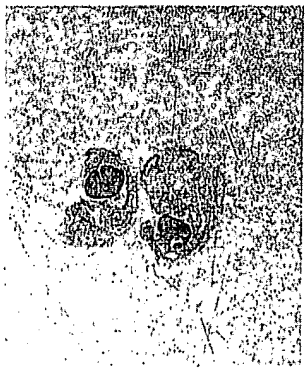
FIG. 3A FIG. 3C FIG. 3E

anti-sense probe





sense probe



day 8.5 - 9.0 day 13.5 day 16.5

FIG. 3B FIG. 3D FIG. 3F

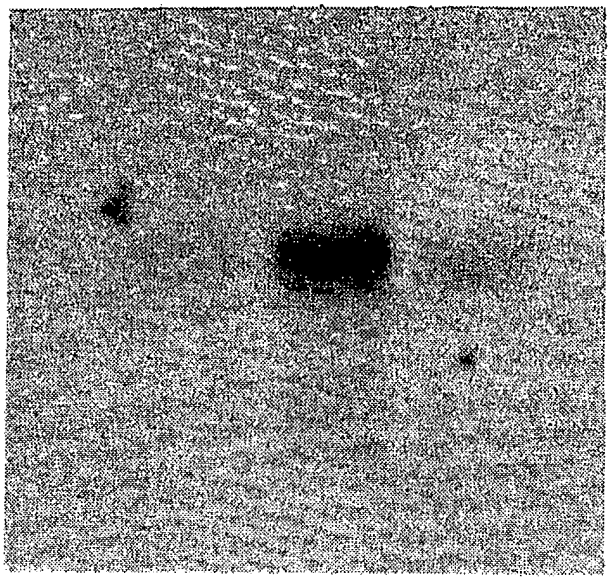


FIG. 4

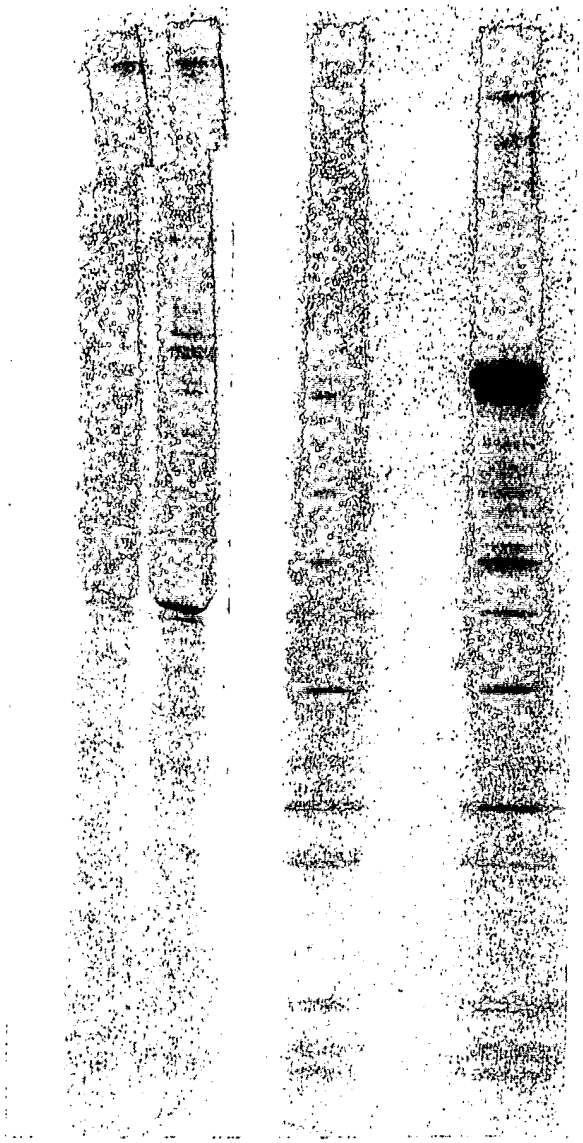


FIG. 5

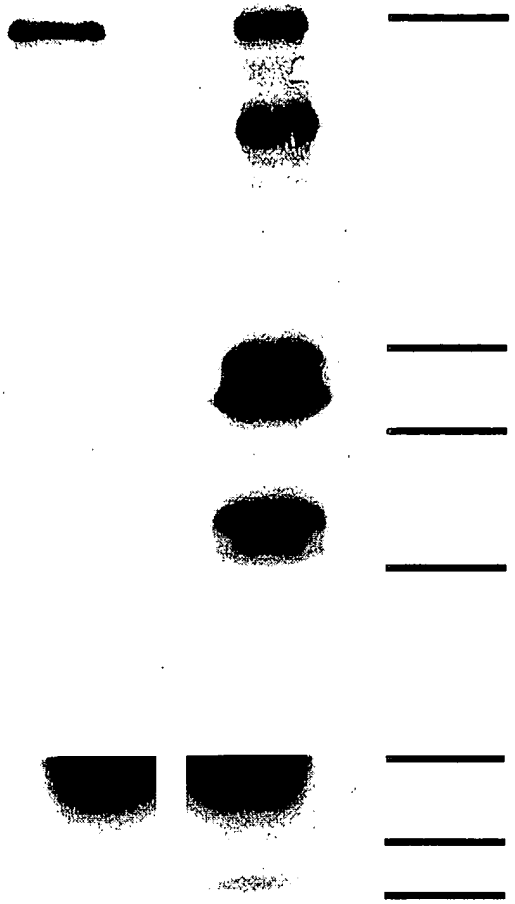


FIG. 6

```
ATGGAGAGCA CCTCCCCGCG AGGTCTCCGG TGCCCACAGC TCTGCAGCCA CTCTGGCGCC ATGAGAGCGC CGACCACCGC   80
TCGCTGCTCC GGATGCATCC AACGGGTGCG TTGGAGGGGC TTCCTGCCAC TTGTCCTGGC TGTCTTGATG GGGACAAGTC  160
ATGCCCAACG GGATTCCATA GGGAGATACG AACCAGCTAG CAGGGATGCG AATCGGTTGT GGCACCCCGT GGGCAGCCAC  240
CCCGCAGCGG CTGCAGCCAA GGTGTACAGT CTGTTCCGAG AGCCTGACGC GCCGGTCCCC GGCTTGTCGC CCTCTGAGTG  320
GAACCAGCCG GCCCAGGGGA ACCCGGGATG GCTCGCAGAG GCCGAGGCCA GGAGGCCACC TCGAACCCAG CAGCTGCGTC  400
GAGTCCAGCC ACCTGTCCAG ACTCGGAGAA GCCATCCCCG GGGCCAGCAG CAGATAGCAG CCCGGGCTGC ACCTTCTGTC  480
GCGCGCCTGG AAACCCCTCA GCGACCCGCG GCTGCACGGC GAGGGCGGCT CACTGGGAGA AATGTCTGCG GGGGACAGTG  560
CTGCCCAGGA TGGACAACAT CAAACAGCAC CAACCACTGT ATCAAACCTG TGTGTCAGCC TCCCTGTCAG AACCGAGGCT  640
CCTGCAGCAG GCCCCAGGTC TGCATCTGCC GTTCTGGCTT CCGTGGGGCG CGCTGTGAGG AGGTCATCCC TGAGGAGGAA  720
TTTGACCCTC AGAATGCCAG GCCTGTGCCC AGACGCTCAG TGGAGAGAGC ACCCGGTCCT CACAGAAGCA GTGAGGCCAG  800
AGGAAGTCTA GTGACCAGAA TACAGCCGCT GGTACCACCA CCATCACCAC CTCCATCTCG GCGCCTCAGC CAGCCCTGGC  880
CCCTGCAGCA GCACTCAGGG CCGTCCAGGA CAGTTCGTCG GTATCCGGCC ACTGGTGCCA ATGGCCAGCT GATGTCCAAC  960
GCTTTGCCTT CAGGACTCGA GCTGAGAGAC AGCAGCCCAC AGGCAGCACA TGTGAACCAT CTCTCACCCC CCTGGGGGCT 1040
GAACCTCACC GAGAAAATCA AGAAAATCAA AGTCGTCTTC ACCCCCACCA TCTGCAAGCA GACCTGTGCC CGGGGACGCT 1120
GTGCCAACAG CTGTGAGAAG GGTGACACCA CCACCTTGTA CAGTCAGGGT GGCCATGGGC ATGACCCCAA GTCTGGCTTC 1200
CGTATCTATT TCTGCCAAAT CCCCTGCCTG AATGGTGGCC GCTGCATCGG CCGGGACGAG TGCTGGTGTC CAGCCAACTC 1280
CACAGGAAAG TTCTGCCATC TGCCTGTCCC GCAGCCAGAC AGGGAACCTG CAGGGCGAGG TTCCCGGCAC AGAACCCTGC 1360
TGGAAGGTCC CCTGAAGCAA TCCACCTTCA CGCTGCCTCT CTCTAACCAG CTCGCCTCTG TGAACCCCTC GCTGGTGAAG 1440
GTGCAAATTC ATCACCCGCC TGAGGCCTCT GTGCAGATTC ACCAGGTGGC CCGGGTCCGG GGTGAGCTGG ACCCCGTGCT 1520
GGAGGACAAC AGTGTGGAGA CCAGAGCCTC TCATCGCCCC CACGGCAACC TAGGCCACAG CCCCTGGGCC AGCAACAGCA 1600
TACCCGCTCG GGCCGGAGAG GCCCCTCGGC CACCACCAGT GCTGTCTAGG CATTATGGAC TTCTGGGCCA GTGTTACCTG 1680
AGCACGGTGA ATGGACAGTG TGCTAACCCC CTAGGTAGTC TGACTTCTCA GGAGGACTGC TGTGGCAGTG TGGGGACCTT 1760
CTGGGGGGTG ACCTCCTGTG CTCCCTGCCC ACCCAGACAA GAGGGTCCAG CCTTCCCAGT GATTGAAAAT GGCCAGCTGG 1840
AGTGTCCCCA AGGATACAAG AGACTGAACC TCAGCCACTG CCAAGATATC AATGAGTGCC TGACCCTGGG CCTCTGCAAG 1920
```

FIG. 7

GACTCGGAGT GCGTGAACAC CAGGGGCAGC TACCTGTGCA CCTGCAGGCC TGGCCTCATG CTGGATCCGT CAAGGAGCCG 2000
CTGCGTATCG GACAAGGCTG TCTCCATGCA GCAGGGACTA TGCTACCGGT CACTGGGGTC TGGTACCTGC ACCCTGCCTT 2080
TGGTTCATCG GATCACCAAG CAGATATGCT GCTGCAGCCG TGTGGGCAAA GCCTGGGGTA GCACATGTGA ACAGTGTCCC 2160
CTGCCTGGCA CAGAAGCCTT CAGGGAGATC TGCCCTGCTG GCCATGGCTA CACCTACTCG AGCTCAGACA TCCGCCTGTC 2240
TATGAGGAAA GCCGAAGAAG AGGAACTGGC TAGCCCCTTA AGGGAGCAGA CAGAGCAGAG CACTGCACCC CCACCTGGGC 2320
AAGCAGAGAG GCAACCACTC CGGGCAGCCA CCGCCACCTG GATTGAGGCT GAGACCCTCC CTGACAAAGG TGACTCTCGG 2400
GCTGTTCAGA TCACAACCAG TGCTCCCCAC CTACCTGCCC GGGTACCAGG GGATGCCACT GGAAGACCAG CACCATCCTT 2480
GCCTGGACAG GGCATTCCAG AGAGTCCAGC AGAAGAGCAA GTGATTCCCT CCAGTGATGT CTTGGTGACA CACAGCCCCC 2560
CAGACTTTGA TCCATGTTTT GCTGGAGCCT CCAACATCTG TGGCCCTGGG ACCTGTGTGA GCCTCCCAAA TGGATACAGA 2640
TGTGTCTGCA GCCCTGGCTA CCAGCTACAC CCCAGCCAAG ACTACTGTAC TGATGACAAC GAGTGTATGA GGAACCCCTG 2720
TGAAGGAAGA GGGCGCTGTG TCAACAGTGT GGGCTCCTAC TCCTGCCTCT GCTATCCTGG CTACACACTA GTCACCCTCG 2800
GAGACACACA GGAGTGCCAA GATATCGATG AGTGTGAGCA GCCCGGGGTG TGCAGTGGTG GGCGATGCAG CAACACGGAG 2880
GGCTCGTACC ACTGCGAGTG TGATCGGGGC TACATCATGG TCAGGAAAGG ACACTGTCAA GATATCAACG AATGCCGTCA 2960
CCCTGGTACC TGCCCTGATG GGAGATGCGT CAACTCCCCT GGCTCCTACA CTTGTCTGGC CTGTGAGGAG GGCTATGTAG 3040
GCCAGAGTGG GAGCTGTGTA GATGTCAATG AGTGTCTGAC CCCTGGGATA TGTACCCATG GAAGGTGCAT CAACATGGAA 3120
GGCTCCTTTA GATGCTCCTG TGAGCCGGGC TATGAGGTCA CCCCAGACAA GAAGGGCTGC CGAGATGTGG ACGAGTGTGC 3200
CAGCCGAGCC TCGTGCCCCA CGGGCCTCTG CCTCAACACG GAGGGCTCCT TCACCTGCTC AGCCTGTCAG AGCGGGTACT 3280
GGGTGAACGA AGATGGCACT GCCTGTGAAG ACTTGGATGA ATGTGCCTTC CCTGGAGTCT GCCCCACAGG CGTCTGCACC 3360
AATACTGTAG GCTCCTTCTC CTGCAAGGAC TGTGACCAGG GCTACCGGCC CAACCCCCTG GGCAACAGAT GCGAAGATGT 3440
GGATGAGTGT GAAGGTCCCC AAAGCAGCTG CCGGGGAGGC GAATGCAAGA ACACAGAAGG TTCCTACCAA TGCCTCTGTC 3520
ACCAGGGCTT CCAGCTGGTC AATGGCACCA TGTGTGAGGA CGTGAATGAG TGTGTTGGGG AAGAGCATTG TGCTCCTCAC 3600
GGCGAGTGCC TCAACAGCCT GGGCTCCTTC TTCTGCCTCT GTGCACCCGG CTTTGCTAGT GCTGAGGGGG GCACCAGATG 3680
CCAGGATGTT GATGAATGTG CAGCCACAGA CCCGTGTCCG GGAGGACACT GTGTCAACAC AGAGGGCTCC TTCAGCTGTC 3760
TGTGTGAGAC TGCTTCCTTC CAGCCCTCCC CAGACAGCGG AGAATGTTTG GATATTGATG AGTGTGAGGA CCGTGAAGAC 3840

FIG. 7.1

CCGGTGTGCG GAGCCTGGAG GTGTGAGAAC AGTCCTGGTT CCTACCGCTG CATCCTGGAC TGCCAGCCTG GATTCTATGT 3920
GGCGCCAAAT GGAGACTGCA TTGACATAGA TGAATGTGCC AATGACACTG TGTGTGGGAA CCATGGCTTC TGTGACAACA 4000
CGGACGGCTC CTTCCGCTGC CTGTGTGACC AGGGCTTCGA GACCTCACCA TCAGGCTGGG AGTGTGTTGA TGTGAACGAG 4080
TGTGAGCTCA TGATGGCAGT GTGTGGGGAT GCGCTCTGTG AGAACGTGGA AGGCTCCTTC CTGTGCCTTT GCGCCAGTGA 4160
CCTTGAGGAG TACGACGCAG AAGAAGGACA CTGCCGTCCT CGGGTGGCTG GAGCTCAGAG AATCCCAGAG GTCCGGACAG 4240
AGGACCAGGC TCCAAGCCTT ATCCGCATGG AATGCTACTC TGAACACAAT GGTGGTCCTC CCTGCTCTCA AATCCTGGGC 4320
CAGAACTCCA CACAGGCCGA GTGCTGCTGC ACTCAGGGTG CCAGATGGGG AAAGGCCTGT GCGCCCTGCC CATCTGAGGA 4400
CTCAGTTGAA TTCAGTCAGC TCTGCCCCAG TGGTCAAGGT TACATCCCAG TGGAAGGAGC CTGGACATTT GGACAAACCA 4480
TGTATACAGA TGCCGATGAA TGTGTACTGT TTGGGCCTGC TCTCTGCCAG AATGGCCGAT GCTCAAACAT AGTGCCTGGC 4560
TACATTTGCC TGTGCAACCC TGGCTACCAC TATGATGCCT CCAGCAGGAA GTGCCAGGAT CACAACGAAT GCCAGGACTT 4640
GGCCTGTGAG AACGGTGAGT GTGTGAACCA AGAAGGCTCC TTCCATTGCC TCTGCAATCC CCCCCTCACC CTAGACCTCA 4720
GTGGGCAGCG CTGTGTGAAC ACGACCAGCA GCACGGAGGA CTTCCCTGAC CATGACATCC ACATGGACAT CTGCTGGAAA 4800
AAAGTCACCA ATGATGTGTG CAGCCAGCCC TTGCGTGGGC ACCATACCAC CTATACAGAA TGCTGCTGCC AAGATGGGGA 4880
GGCCTGGAGC CAGCAATGCG CTCTGTGCCC GCCCAGGAGC TCTGAGGTCT ACGCTCAGCT GTGCAACGTG GCTCGGATTG 4960
AGGCAGAGCG CGGAGCAGGG ATCCACTTCC GGCCAGGCTA TGAGTATGGC CCTGGCCTGG ACGATCTGCC TGAAAACCTC 5040
TACGGCCCAG ATGGGGCTCC CTTCTATAAC TACCTAGGCC CCGAGGACAC TGCCCCTGAG CCTCCCTTCT CCAACCCAGC 5120
CAGCCAGCCG GGAGACAACA CACCTGTCCT TGAGCCTCCT CTGCAGCCCT CTGAACTTCA GCCTCACTAT CTAGCCAGCC 5200
ACTCAGAACC CCCTGCCTCC TTCGAAGGCC TTCAGGCTGA GGAATGTGGC ATCCTGAATG GCTGTGAGAA TGGCCGCTGC 5280
GTGCGTGTGC GGGAGGGCTA CACTTGCGAC TGCTTTGAGG GCTTCCAGCT GGATGCGCCC ACATTGGCCT GTGTGGATGT 5360
GAACGAGTGT GAAGACTTGA ACGGGCCTGC ACGACTCTGT GCACACGGTC ACTGTGAGAA CACAGAGGGT TCCTATCGCT 5440
GCCACTGTTC GCCAGGTTAC GTGGCAGAGC CAGGCCCCCC ACACTGTGCG GCCAAGGAGT AG 5502

FIG.7.2

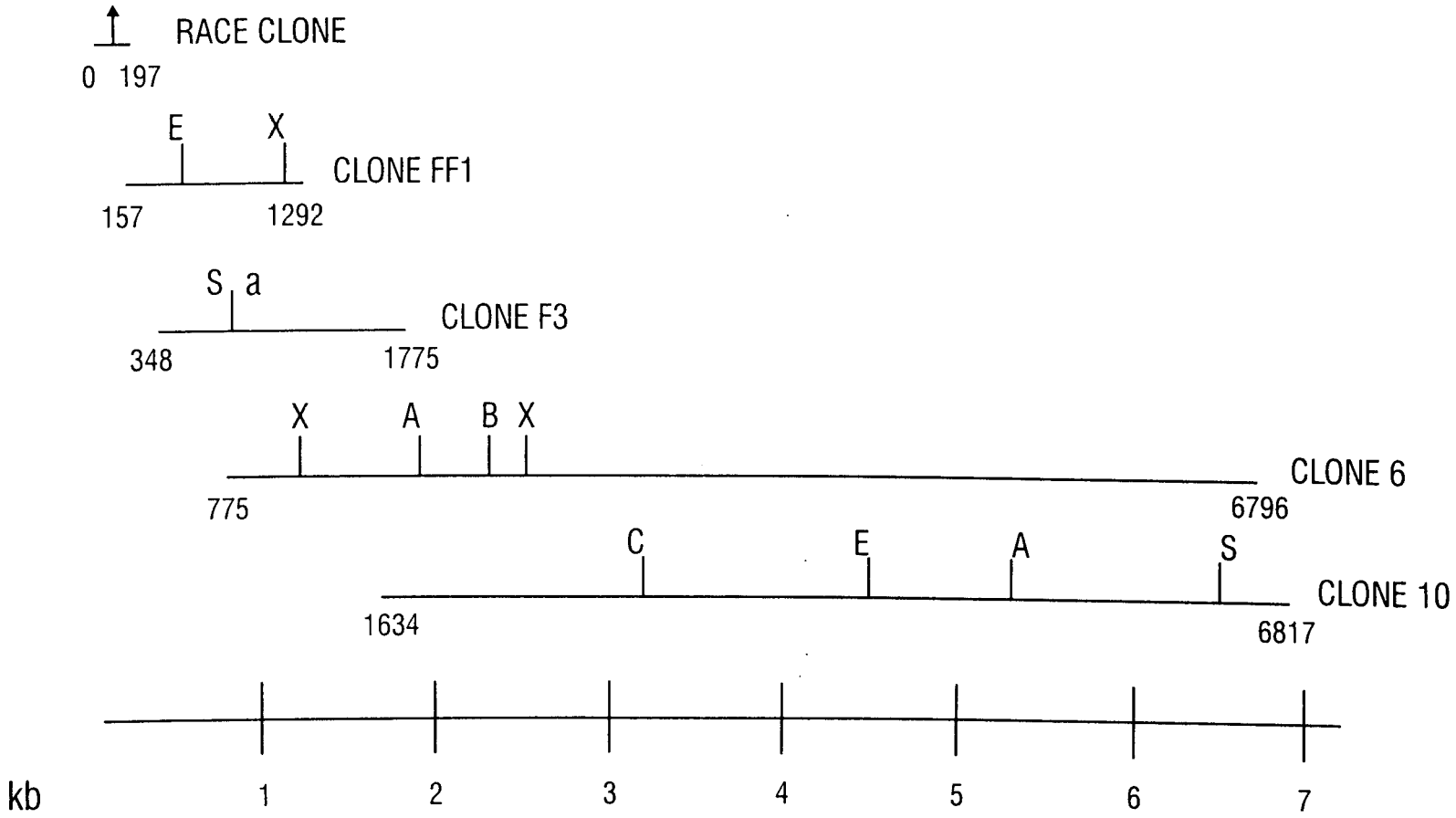

RACE CLONE
0 197
E X
CLONE FF1
157 1292
S a
CLONE F3
348 1775
X A B X
CLONE 6
775 6796
C E A S
CLONE 10
1634 6817
kb
1 2 3 4 5 6 7

FIG. 7

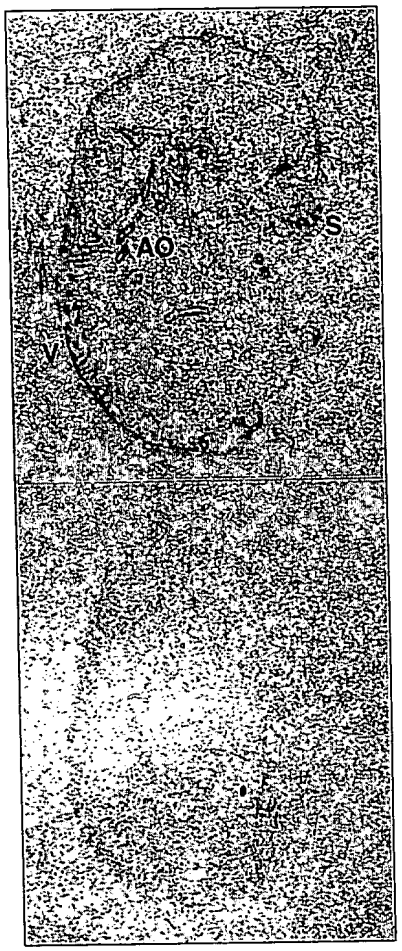


FIG. 8A

FIG. 8B

FIG. 8C

MESTSPRGLRCPQLCSHSGAMRAPTTARCSGCIQRVRWRGFLPLVLAVLMGTSHAQRDSIGRYEPASRDANRLWHPVGSHPAAAAAKVYS	90
LFREPDAPVPGLSPSEWNQPAQGNPGWLAEAEARRPPRTQQLRRVQPPVQTRRSHPRGQQQIAARAAPSVARLETPQRPAAARRGRLTGR	180
NVCGGQCCPGWTTSNSTNHCIKPVCQPPCQNRGSCSRPQVCICRSGFRGARCEEVIPEEEFDPQNARPVPRRSVERAPGPHRSSEARGSL	270
VTRIQPLVPPPSPPPSRRLSQPWPLQQHSGPSRTVRRYPATGANGQLMSNALPSGLELRDSSPQAAHVNHLSPPWGLNLTEKIKKIKVVF	360
TPTICKQTCARGRCANSCEKGDTTTLYSQGGHGHDPKSGFRIYFCQIPCLNGGRCIGRDECWCPANSTGKFCHLPVPQPDREPAGRGSRH	450
RTLLEGPLKQSTFTLPLSNQLASVNPSLVKVQIHHPPEASVQIHQVARVRGELDPVLEDNSVETRASHRPHGNLGHSPWASNSIPARAGE	540
APRPPPVLSRHYGLLGQCYLSTVNGQCANPLGSLTSQEDCCGSVGTFWGVTSCAPCPPRQEGPAFPVIENGQLECPQGYKRLNLSHCQDI	630
NECLTLGLCKDSECVNTRGSYLCTCRPGLMLDPSRSRCVSDKAVSMQQGLCYRSLGSGTCTLPLVHRITKQICCCSRVGKAWGSTCEQCP	720
LPGTEAFREICPAGHGYTYSSSDIRLSMRKAEEEELASPLREQTEQSTAPPPGQAERQPLRAATATWIEAETLPDKGDSRAVQITTSAPH	810
LPARVPGDATGRPAPSLPGQGIPESPAEEQVIPSSDVLVTHSPPDFDPCFAGASNICGPGTCVSLPNGYRCVCSPGYQLHPSQDYCTDDN	900
ECMRNPCEGRGRCVNSVGSYSCLCYPGYTLVTLGDTQECQDIDECEQPGVCSGGRCSNTEGSYHCECDRGYIMVRKGHCQDINECRHPGT	990
CPDGRCVNSPGSYTCLACEEGYVGQSGSCVDVNECLTPGICTHGRCINMEGSFRCSCEPGYEVTPDKKGCRDVDECASRASCPTGLCLNT	1080
EGSFTCSACQSGYWVNEDGTACEDLDECAFPGVCPTGVCTNTVGSFSCKDCDQGYRPNPLGNRCEDVDECEGPQSSCRGGECKNTEGSYQ	1170
CLCHQGFQLVNGTMCEDVNECVGEEHCAPHGECLNSLGSFFCLCAPGFASAEGGTRCQDVDECAATDPCPGGHCVNTEGSFSCLCETASF	1260
QPSPDSGECLDIDECEDREDPVCGAWRCENSPGSYRCILDCQPGFYVAPNGDCIDIDECANDTVCGNHGFCDNTDGSFRCLCDQGFETSP	1350
SGWECVDVNECELMMAVCGDALCENVEGSFLCLCASDLEEYDAEEGHCRPRVAGAQRIPEVRTEDQAPSLIRMECYSEHNGGPPCSQILG	1440
QNSTQAECCCTQGARWGKACAPCPSEDSVEFSQLCPSGQGYIPVEGAWTFGQTMYTDADECVLFGPALCQNGRCSNIVPGYICLCNPGYH	1530
YDASSRKCQDHNECQDLACENGECVNQEGSFHCLCNPPLTLDLSGQRCVNTTSSTEDFPDHDIHMDICWKKVTNDVCSQPLRGHHTTYTE	1620
CCCQDGEAWSQQCALCPPRSSEVYAQLCNVARIEAERGAGIHFRPGYEYGPGLDDLPENLYGPDGAPFYNYLGPEDTAPEPPFSNPASQP	1710
GDNTPVLEPPLQPSELQPHYLASHSEPPASFEGLQAEECGILNGCENGRCVRVREGYTCDCFEGFQLDAPTLACVDVNECEDLNGPARLC	1800
AHGHCENTEGSYRCHCSPGYVAEPGPPHCAAKE	1833

FIG. 8

```
ATG CGC CAG GCC GCA TTG GGG CTG CTG GCA CTA CTC CTG CTG GCG CTG CTG GGC 54
 M   R   Q   A   A   L   G   L   L   A   L   L   L   L   A   L   L   G  18

CCC GGC GGC CGA GGG GTG GGC CGG CCG GGC AGC GGG GCA CAG GCG GGG GCG GGG 108
 P   G   G   R   G   V   G   R   P   G   S   G   A   Q   A   G   A   G  36

CGC TGG GCC CAA CGC TTC AAG GTG GTC TTT GCG CCT GTG ATC TGC AAG CGG ACC 162
 R   W   A   Q   R   F   K   V   V   F   A   P   V   I   C   K   R   T  54

TGT CTG AAG GGC CAG TGT CGG GAC AGC TGT CAG CAG GGC TCC AAC ATG ACG CTC 216
 C   L   K   G   Q   C   R   D   S   C   Q   Q   G   S   N   M   T   L  72

ATC GGA GAG AAC GGC CAC AGC ACC GAC ACG CTC ACC GGT TCT GCC TTC CGC GTG 270
 I   G   E   N   G   H   S   T   D   T   L   T   G   S   A   F   R   V  90

GTG GTG TGC CCT CTA CCC TGC ATG AAC GGT GGC CAG TGC TCT TCC CGA AAC CAG 324
 V   V   C   P   L   P   C   M   N   G   G   Q   C   S   S   R   N   Q 108

TGC CTG TGT CCC CCG GAT TTC ACG GGG CGC TTC TGC CAG GTG CCT GCT GCA GGA 378
 C   L   C   P   P   D   F   T   G   R   F   C   Q   V   P   A   A   G 126

ACC GGA GCT GGC ACC GGG AGT TCA GGC CCC GGC TGG CCC GAC CGG GCC ATG TCC 432
 T   G   A   G   T   G   S   S   G   P   G   W   P   D   R   A   M   S 144

ACA GGC CCG CTG CCG CCC CTT GCC CCA GAA GGA GAG TCT GTG GCT AGC AAA CAC 486
 T   G   P   L   P   P   L   A   P   E   G   E   S   V   A   S   K   H 162

GCC ATT TAC GCG GTG CAG GTG ATC GCA GAT CCT CCC GGG CCG GGG GAG GGT CCT 540
 A   I   Y   A   V   Q   V   I   A   D   P   P   G   P   G   E   G   P 180

CCT GCA CAA CAT GCA GCC TTC TTG GTG CCC CTG GGG CCA GGA CAA ATC TCG GCA 594
 P   A   Q   H   A   A   F   L   V   P   L   G   P   G   Q   I   S   A 198

GAA GTG CAG GCT CCG CCC CCC GTG GTG AAC GTG CGT GTC CAT CAC CCT CCT GAA 648
 E   V   Q   A   P   P   P   V   V   N   V   R   V   H   H   P   P   E 216

GCT TCC GTT CAG GTG CAC CGC ATC GAG GGG CCG AAC GCT GAA GGC CCA GCC TCT 702
 A   S   V   Q   V   H   R   I   E   G   P   N   A   E   G   P   A   S 234

TCC CAG CAC TTG CTG CCG CAT CCC AAG CCC CAG CAC CCG AGG CCA CCC ACT CAA 756
 S   Q   H   L   L   P   H   P   K   P   Q   H   P   R   P   P   T   Q 252

AAG CCA CTG GGC CGC TGC TTC CAG GAC ACA TTG CCC AAG CAG CCT TGT GGC AGC 810
 K   P   L   G   R   C   F   Q   D   T   L   P   K   Q   P   C   G   S 270

AAC CCT TTG CCT GGC CTT ACC AAG CAG GAA GAT TGC TGC GGT AGC ATC GGT ACT 864
 N   P   L   P   G   L   T   K   Q   E   D   C   C   G   S   I   G   T 288

GCC TGG GGA CAA AGC AAG TGT CAC AAG TGC CCA CAG CTT CAG TAT ACA GGG GTG 918
 A   W   G   Q   S   K   C   H   K   C   P   Q   L   Q   Y   T   G   V 306

CAG AAG CCT GTA CCT GTA CGT GGG GAG GTG GGT GCT GAC TGC CCC CAG GGC TAC 972
 Q   K   P   V   P   V   R   G   E   V   G   A   D   C   P   Q   G   Y 324

AAG AGG CTC AAC AGC ACC CAC TGC CAG GAT ATC AAC GAA TGT GCG ATG CCC GGG 1026
 K   R   L   N   S   T   H   C   Q   D   I   N   E   C   A   M   P   G 342
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FIG. 9

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AAT GTG TGC CAT GGT GAC TGC CTC AAC AAC CCT GGC TCT TAT CGC TGT GTC TGC 1080
 N   V   C   H   G   D   C   L   N   N   P   G   S   Y   R   C   V   C  360

CCG CCC GGT CAT AGC TTG GGT CCC CTC GCA GCA CAG TGC ATT GCC GAC AAA CCA 1134
 P   P   G   H   S   L   G   P   L   A   A   Q   C   I   A   D   K   P  378

GAG GAG AAG AGC CTG TGT TTC CGC CTT GTG AGC ACC GAA CAC CAG TGC CAG CAC 1188
 E   E   K   S   L   C   F   R   L   V   S   T   E   H   Q   C   Q   H  396

CCT CTG ACC ACA CGC CTA ACC CGC CAG CTC TGC TGC TGT AGT GTG GGT AAA GCC 1242
 P   L   T   T   R   L   T   R   Q   L   C   C   C   S   V   G   K   A  414

TGG GGT GCC CGG TGC CAG CGC TGC CCG GCA GAT GGT ACA GCA GCC TTC AAG GAG 1296
 W   G   A   R   C   Q   R   C   P   A   D   G   T   A   A   F   K   E  432

ATC TGC CCC GGC TGG GAA AGG GTA CCA TAT CCT CAC CTC CCA CCA GAC GCT CAC 1350
 I   C   P   G   W   E   R   V   P   Y   P   H   L   P   P   D   A   H  450

CAT CCA GGG GGA AAG CGA CTT CTC CCT CTT CCT GCA CCC GAC GGG CCA CCC AAA 1404
 H   P   G   G   K   R   L   L   P   L   P   A   P   D   G   P   P   K  468

CCC CAG CAG CTT CCT GAA AGC CCC AGC CGA GCA CCA CCC CTC GAG GAC ACA GAG 1458
 P   Q   Q   L   P   E   S   P   S   R   A   P   P   L   E   D   T   E  486

GAA GAG AGA GGA GTG ACC ATG GAT CCA CCA GTG AGT GAG GAG CGA TCG GTG CAG 1512
 E   E   R   G   V   T   M   D   P   P   V   S   E   E   R   S   V   Q  504

CAG AGC CAC CCC ACT ACC ACC ACC TCA CCC CCC CGG CCT TAC CCA GAG CTC ATC 1566
 Q   S   H   P   T   T   T   T   S   P   P   R   P   Y   P   E   L   I  522

TCT CGC CCC TCC CCA CCT ACC TTC CAC CGG TTC CTG CCA GAC TTG CCC CCA TCC 1620
 S   R   P   S   P   P   T   F   H   R   F   L   P   D   L   P   P   S  540

CGA AGT GCA GTG GAG ATC GCC CCC ACT CAG GTC ACA GAG ACC GAT GAG TGC CGA 1674
 R   S   A   V   E   I   A   P   T   Q   V   T   E   T   D   E   C   R  558

TTG AAC CAG AAT ATC TGT GGC CAT GGA CAG TGT GTG CCT GGC CCC TCG GAT TAC 1728
 L   N   Q   N   I   C   G   H   G   Q   C   V   P   G   P   S   D   Y  576

TCC TGC CAC TGC AAC GCT GGC TAC CGG TCA CAC CCG CAG CAC CGC TAC TGT GTT 1782
 S   C   H   C   N   A   G   Y   R   S   H   P   Q   H   R   Y   C   V  594

GAT GTG AAC GAG TGC GAG GCA GAG CCC TGC GGC CCC GGG AAA GGC ATC TGT ATG 1836
 D   V   N   E   C   E   A   E   P   C   G   P   G   K   G   I   C   M  612

AAC ACT GGT GGC TCC TAC AAT TGT CAC TGC AAC CGA GGC TAC CGC CTC CAC GTG 1890
 N   T   G   G   S   Y   N   C   H   C   N   R   G   Y   R   L   H   V  630

GGT GCA GGG GGC CGC TCG TGC GTG GAC CTG AAC GAG TGC GCC AAG CCT CAC CTG 1944
 G   A   G   G   R   S   C   V   D   L   N   E   C   A   K   P   H   L  648

TGT GGG GAC GGT GGC TTC TGC ATC AAC TTC CCT GGT CAC TAC AAA TGC AAC TGC 1998
 C   G   D   G   G   F   C   I   N   F   P   G   H   Y   K   C   N   C  666

TAT CCT GGC TAC CGG CTC AAG GCC TCC CGA CCG CCC ATT TGC GAA GAC ATC GAC 2052
 Y   P   G   Y   R   L   K   A   S   R   P   P   I   C   E   D   I   D  684

GAG TGT CGC GAC CCT AGC ACC TGC CCT GAT GGC AAA TGT GAA AAC AAA CCT GGC 2106
 E   C   R   D   P   S   T   C   P   D   G   K   C   E   N   K   P   G  702
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FIG. 9.1

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AGC TTC AAG TGC ATC GCC TGC CAG CCT GGC TAC CGT AGC CAG GGG GGC GGG GCC 2160
 S   F   K   C   I   A   C   Q   P   G   Y   R   S   Q   G   G   G   A  720

TGT CGT GAT GTC AAC GAA TGC TCC GAA GGT ACC CCC TGC TCT CCT GGA TGG TGT 2214
 C   R   D   V   N   E   C   S   E   G   T   P   C   S   P   G   W   C  738

GAG AAA CTT CCG GGT TCT TAC CGT TGC ACG TGT GCC CAG GGG ATA CGA ACC CGC 2268
 E   K   L   P   G   S   Y   R   C   T   C   A   Q   G   I   R   T   R  756

ACA GGA CGC CTC AGT TGC ATA GAC GTG GAT GAC TGT GAG GCT GGG AAA GTG TGC 2322
 T   G   R   L   S   C   I   D   V   D   D   C   E   A   G   K   V   C  774

CAA GAT GGC ATC TGC ACG AAC ACA CCA GGC TCT TTC CAG TGT CAG TGC CTC TCC 2376
 Q   D   G   I   C   T   N   T   P   G   S   F   Q   C   Q   C   L   S  792

GGC TAT CAT CTG TCA AGG GAT CGG AGC CGC TGT GAG GAC ATT GAT GAA TGT GAC 2430
 G   Y   H   L   S   R   D   R   S   R   C   E   D   I   D   E   C   D  810

TTC CCT GCG GCC TGC ATC GGG GGT GAC TGC ATC AAT ACC AAT GGT TCC TAC AGA 2484
 F   P   A   A   C   I   G   G   D   C   I   N   T   N   G   S   Y   R  828

TGT CTC TGT CCC CTG GGT CAT CGG TTG GTG GGC GGC AGG AAG TGC AAG AAA GAT 2538
 C   L   C   P   L   G   H   R   L   V   G   G   R   K   C   K   K   D  846

ATA GAT GAG TGC AGC CAG GAC CCA GGC CTG TGC CTG CCC CAT GCC TGC GAG AAC 2592
 I   D   E   C   S   Q   D   P   G   L   C   L   P   H   A   C   E   N  864

CTC CAG GGC TCC TAT GTC TGT GTC TGT GAT GAG GGT TTC ACA CTC ACC CAG GAC 2646
 L   Q   G   S   Y   V   C   V   C   D   E   G   F   T   L   T   Q   D  882

CAG CAT GGG TGT GAG GAG GTG GAG CAG CCC CAC CAC AAG AAG GAG TGC TAC CTT 2700
 Q   H   G   C   E   E   V   E   Q   P   H   H   K   K   E   C   Y   L  900

AAC TTC GAT GAC ACA GTG TTC TGT GAC AGC GTA TTG GCT ACC AAT GTC ACT CAG 2754
 N   F   D   D   T   V   F   C   D   S   V   L   A   T   N   V   T   Q  918

CAG GAA TGC TGT TGC TCT CTG GGA GCT GGC TGG GGA GAC CAC TGC GAA ATC TAT 2808
 Q   E   C   C   C   S   L   G   A   G   W   G   D   H   C   E   I   Y  936

CCC TGT CCA GTC TAC AGC TCA GCC GAA TTT CAC AGC CTG GTG CCT GAT GGG AAA 2862
 P   C   P   V   Y   S   S   A   E   F   H   S   L   V   P   D   G   K  954

AGG CTA CAC TCA GGA CAA CAA CAT TGT GAA CTA TGC ATT CCT GCC CAC CGT GAC 2916
 R   L   H   S   G   Q   Q   H   C   E   L   C   I   P   A   H   R   D  972

ATC GAC GAA TGC ATA TTG TTT GGG GCA GAG ATC TGC AAG GAG GGC AAG TGT GTG 2970
 I   D   E   C   I   L   F   G   A   E   I   C   K   E   G   K   C   V  990

AAC TCG CAG CCC GGC TAC GAG TGC TAC TGC AAG CAG GGC TTC TAC TAC GAT GGC 3024
 N   S   Q   P   G   Y   E   C   Y   C   K   Q   G   F   Y   Y   D   G 1008

AAC CTG CTG GAG TGC GTG GAC GTG GAC GAG TGC TTG GAT GAG TCT AAC TGC AGG 3078
 N   L   L   E   C   V   D   V   D   E   C   L   D   E   S   N   C   R 1026

AAC GGA GTG TGT GAG AAC ACG TGG CGG CTA CCG TGT GCC TGC ACT CCG CCG GCA 3132
 N   G   V   C   E   N   T   W   R   L   P   C   A   C   T   P   P   A 1044

GAG TAC AGT CCC GCA CAG GCC CAG TGT CTG AGC CCG GAG GAG ATG GAG CAC GCC 3186
 E   Y   S   P   A   Q   A   Q   C   L   S   P   E   E   M   E   H   A 1062
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FIG. 9.2

CCA GAG AGA CGT GAA GTG TGC TGG GGC CAG CGA GGA GAG GAC GGC ATG TGT ATG 3240

P E R R E V C W G Q R G E D G M C M 1080

GGG CCC CTG GCG GGA CCT GCC CTC ACT TTT GAT GAC TGC TGC TGC CGC CAG CCG 3294

G P L A G P A L T F D D C C C R Q P 1098

CGG CTG GGG TAC CAG TGC AGA CCG TGC CCG CCA CGT GGC ACC GGG TCC CAG TGC 3348

R L G Y Q C R P C P P R G T G S Q C 1116

CCG ACT TCA CAG AGT GAG AGC AAT TCT TTC TGG GAC ACA AGC CCC CTG CTA CTG 3402

P T S Q S E S N S F W D T S P L L L 1134

GGG AAG TCT CCG CGA GAC GAA GAC AGC TCA GAG GAG GAT TCA GAT GAG TGC CGT 3456

G K S P R D E D S S E E D S D E C R 1152

TGT GTG AGC GGA CCG TGT GTG CCA CGG CCA GGC GGG GCG GTA TGC GAG TGT CCT 3510

C V S G P C V P R P G G A V C E C P 1170

GGA GGC TTT CAG CTG GAC GCC TCC CGT GCC CGC TGC GTG GAC ATT GAT GAG TGC 3564

G G F Q L D A S R A R C V D I D E C 1188

CGA GAA CTG AAC CAG CGG GGA CTG CTG TGT AAG AGC GAG CGG TGC GTG AAC ACC 3618

R E L N Q R G L L C K S E R C V <u>N T</u> 1206

AGT GGA TCC TTC CGC TGT GTC TGC AAA GCT GGC TTC ACG CGC AGC CGC CCT CAC 3672

<u>S</u> G S F R C V C K A G F T R S R P H 1224

GGG CCT GCG TGC CTC AGC GCC GCC GCT GAT GAT GCA GCC ATA GCC CAC ACC TCA 3726

G P A C L S A A A D D A A I A H T S 1242

GTG ATC GAT CAT CGA GGG TAT TTT CAC TGA

V I D H R G Y F H *

FIG. 9.3

Met Arg Gln Ala Ala Leu Gly Leu Leu Ala Leu Leu Leu Leu Ala Leu Leu Gly Pro Gly Gly Arg	22
Gly Val Gly Arg Pro Gly Ser Gly Ala Gln Ala Gly Ala Gly Arg Trp Ala Gln Arg Phe Lys Val	44
Val Phe Ala Pro Val Ile Cys Lys Arg Thr Cys Leu Lys Gly Gln Cys Arg Asp Ser Cys Gln Gln	66
Gly Ser Asn Met Thr Leu Ile Gly Glu Asn Gly His Ser Thr Asp Thr Leu Thr Gly Ser Ala Phe	88
Arg Val Val Val Cys Pro Leu Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asn Gln Cys Leu	110
Cys Pro Pro Asp Phe Thr Gly Arg Phe Cys Gln Val Pro Ala Ala Gly Thr Gly Ala Gly Thr Gly	132
Ser Ser Gly Pro Gly Trp Pro Asp Arg Ala Met Ser Thr Gly Pro Leu Pro Pro Leu Ala Pro Glu	154
Gly Glu Ser Val Ala Ser Lys His Ala Ile Tyr Ala Val Gln Val Ile Ala Asp Pro Pro Gly Pro	176
Gly Glu Gly Pro Pro Ala Gln His Ala Ala Phe Leu Val Pro Leu Gly Pro Gly Gln Ile Ser Ala	198
Glu Val Gln Ala Pro Pro Pro Val Val Asn Val Arg Val His His Pro Pro Glu Ala Ser Val Gln	220
Val His Arg Ile Glu Gly Pro Asn Ala Glu Gly Pro Ala Ser Ser Gln His Leu Leu Pro His Pro	242
Lys Pro Pro His Pro Arg Pro Pro Thr Gln Lys Pro Leu Gly Arg Cys Phe Gln Asp Thr Leu Pro	264
Lys Gln Pro Cys Gly Ser Asn Pro Leu Pro Gly Leu Thr Lys Gln Glu Asp Cys Cys Gly Ser Ile	286
Gly Thr Ala Trp Gly Gln Ser Lys Cys His Lys Cys Pro Gln Leu Gln Tyr Thr Gly Val Gln Lys	308
Pro Val Pro Val Arg Gly Glu Val Gly Ala Asp Cys Pro Gln Gly Tyr Lys Arg Leu Asn Ser Thr	330
His Cys Gln Asp Ile Asn Glu Cys Ala Met Pro Gly Asn Val Cys His Gly Asp Cys Leu Asn Asn	352
Pro Gly Ser Tyr Arg Cys Val Cys Pro Pro Gly His Ser Leu Gly Pro Leu Ala Ala Gln Cys Ile	374
Ala Asp Lys Pro Glu Glu Lys Ser Leu Cys Phe Arg Leu Val Ser Thr Glu His Gln Cys Gln His	396
Pro Leu Thr Thr Arg Leu Thr Arg Gln Leu Cys Cys Cys Ser Val Gly Lys Ala Trp Gly Ala Arg	418
Cys Gln Arg Cys Pro Ala Asp Gly Thr Ala Ala Phe Lys Glu Ile Cys Pro Gly Trp Glu Arg Val	440
Pro Tyr Pro His Leu Pro Pro Asp Ala His His Pro Gly Gly Lys Arg Leu Leu Pro Leu Pro Ala	462
Pro Asp Gly Pro Pro Lys Pro Gln Gln Leu Pro Glu Ser Pro Ser Arg Ala Pro Pro Leu Glu Asp	484

FIG. 10

Thr Glu Glu Glu Arg Gly Val Thr Met Asp Pro Pro Val Ser Glu Glu Arg Ser Val Gln Gln Ser	506
His Pro Thr Thr Thr Thr Ser Pro Pro Arg Pro Tyr Pro Glu Leu Ile Ser Arg Pro Ser Pro Pro	528
Thr Phe His Arg Phe Leu Pro Asp Leu Pro Pro Ser Arg Ser Ala Val Glu Ile Ala Pro Thr Gln	550
Val Thr Glu Thr Asp Glu Cys Arg Leu Asn Gln Asn Ile Cys Gly His Gly Gln Cys Val Pro Gly	572
Pro Ser Asp Tyr Ser Cys His Cys Asn Ala Gly Tyr Arg Ser His Pro Gln His Arg Tyr Cys Val	594
Asp Val Asn Glu Cys Glu Ala Glu Pro Cys Gly Pro Gly Lys Gly Ile Cys Met Asn Thr Gly Gly	616
Ser Tyr Asn Cys His Cys Asn Arg Gly Tyr Arg Leu His Val Gly Ala Gly Gly Arg Ser Cys Val	638
Asp Leu Asn Glu Cys Ala Lys Pro His Leu Cys Gly Asp Gly Gly Phe Cys Ile Asn Phe Pro Gly	660
His Tyr Lys Cys Asn Cys Tyr Pro Gly Tyr Arg Leu Lys Ala Ser Arg Pro Pro Ile Cys Glu Asp	682
Ile Asp Glu Cys Arg Asp Pro Ser Thr Cys Pro Asp Gly Lys Cys Glu Asn Lys Pro Gly Ser Phe	704
Lys Cys Ile Ala Cys Gln Pro Gly Tyr Arg Ser Gln Gly Gly Gly Ala Cys Arg Asp Val Asn Glu	726
Cys Ser Glu Gly Thr Pro Cys Ser Pro Gly Trp Cys Glu Lys Leu Pro Gly Ser Tyr Arg Cys Thr	748
Cys Ala Gln Gly Ile Arg Thr Arg Thr Gly Arg Leu Ser Cys Ile Asp Val Asp Asp Cys Glu Ala	770
Gly Lys Val Cys Gln Asp Gly Ile Cys Thr Asn Thr Pro Gly Ser Phe Gln Cys Gln Cys Leu Ser	792
Gly Tyr His Leu Ser Arg Asp Arg Ser Arg Cys Glu Asp Ile Asp Glu Cys Asp Phe Pro Ala Ala	814
Cys Ile Gly Gly Asp Cys Ile Asn Thr Asn Gly Ser Tyr Arg Cys Leu Cys Pro Leu Gly His Arg	836
Leu Val Gly Gly Arg Lys Cys Lys Lys Asp Ile Asp Glu Cys Ser Gln Asp Pro Gly Leu Cys Leu	858
Pro His Ala Cys Glu Asn Leu Gln Gly Ser Tyr Val Cys Val Cys Asp Glu Gly Phe Thr Leu Thr	880
Gln Asp Gln His Gly Cys Glu Glu Val Glu Gln Pro His His Lys Lys Glu Cys Tyr Leu Asn Phe	902
Asp Asp Thr Val Phe Cys Asp Ser Val Leu Ala Thr Asn Val Thr Gln Gln Glu Cys Cys Cys Ser	924
Leu Gly Ala Gly Trp Gly Asp His Cys Glu Ile Tyr Pro Cys Pro Val Tyr Ser Ser Ala Glu Phe	946
His Ser Leu Val Pro Asp Gly Lys Arg Leu His Ser Gly Gln Gln His Cys Glu Leu Cys Ile Pro	968

FIG. 10.1

```
Ala His Arg Asp Ile Asp Glu Cys Ile Leu Phe Gly Ala Glu Ile Cys Lys Glu Gly Lys Cys Val   990
Asn Ser Gln Pro Gly Tyr Glu Cys Tyr Cys Lys Gln Gly Phe Tyr Tyr Asp Gly Asn Leu Leu Glu  1012
Cys Val Asp Val Asp Glu Cys Leu Asp Glu Ser Asn Cys Arg Asn Gly Val Cys Glu Asn Thr Trp  1034
Arg Leu Pro Cys Ala Cys Thr Pro Pro Ala Glu Tyr Ser Pro Ala Gln Ala Gln Cys Leu Ile Pro  1056
Glu Arg Trp Ser Thr Pro Gln Arg Asp Val Lys Cys Ala Gly Ala Ser Glu Glu Arg Thr Ala Cys  1078
Val Trp Gly Pro Trp Ala Gly Pro Ala Leu Thr Phe Asp Asp Cys Cys Cys Arg Gln Pro Arg Leu  1100
Gly Thr Gln Cys Arg Pro Cys Pro Pro Arg Gly Thr Gly Ser Gln Cys Pro Thr Ser Gln Ser Glu  1122
Ser Asn Ser Phe Trp Asp Thr Ser Pro Leu Leu Leu Gly Lys Ser Pro Arg Asp Glu Asp Ser Ser  1144
Glu Glu Asp Ser Asp Glu Cys Arg Cys Val Ser Gly Pro Cys Val Pro Arg Pro Gly Gly Ala Val  1166
Cys Glu Cys Pro Gly Gly Phe Gln Leu Asp Ala Ser Arg Ala Arg Cys Val Asp Ile Asp Glu Cys  1188
Arg Glu Leu Asn Gln Arg Gly Leu Leu Cys Lys Ser Glu Arg Cys Val Asn Thr Ser Gly Ser Phe  1210
Arg Cys Val Cys Lys Ala Gly Phe Thr Arg Ser Arg Pro His Gly Pro Ala Cys Leu Ser Ala Ala  1232
Ala Asp Asp Ala Ala Ile Ala His Thr Ser Val Ile Asp His Arg Gly Tyr Phe His             1251
```

FIG. 10.2

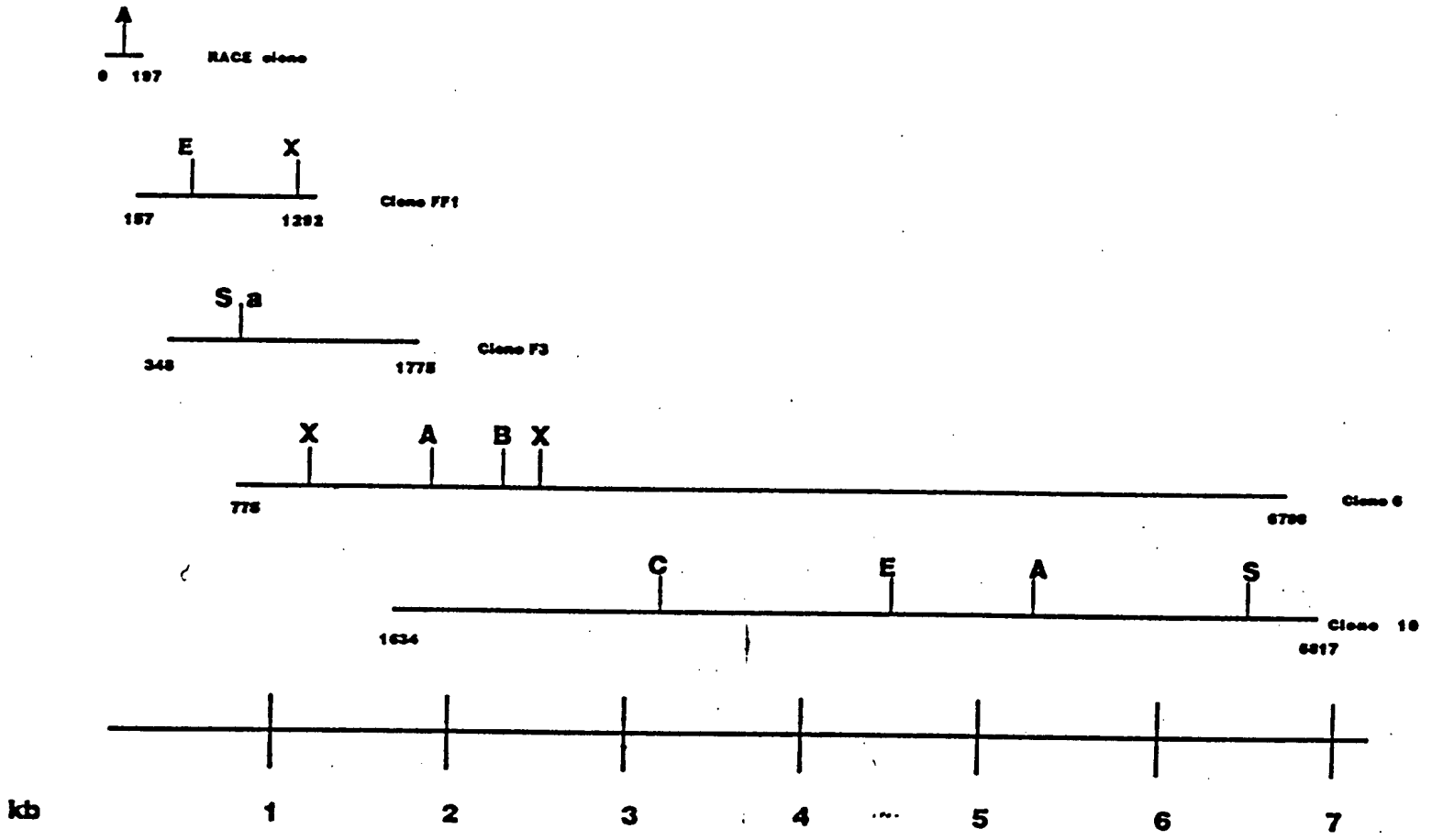
A
RACE clone
0 197
E X
Clone FF1
157 1292
S a
Clone F3
348 1775
X A B X
775
6700
Clone 6
C E A S
1634
6917
Clone 10
kb
1 2 3 4 5 6 7

FIG. 11

FIG. 12A

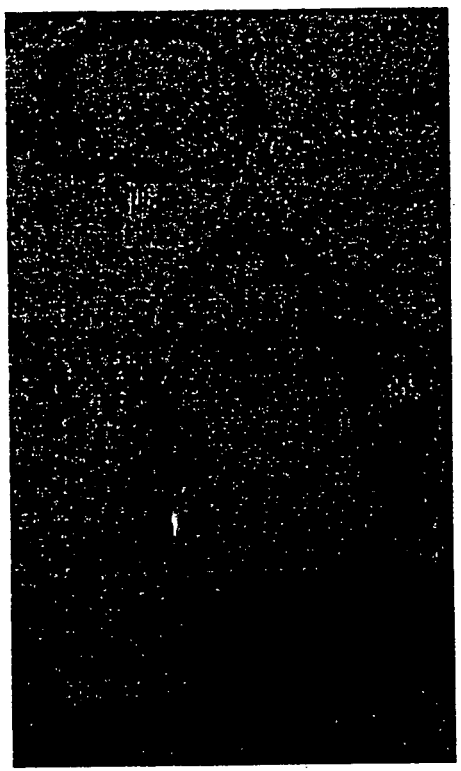

FIG. 12B

FIG. 12C

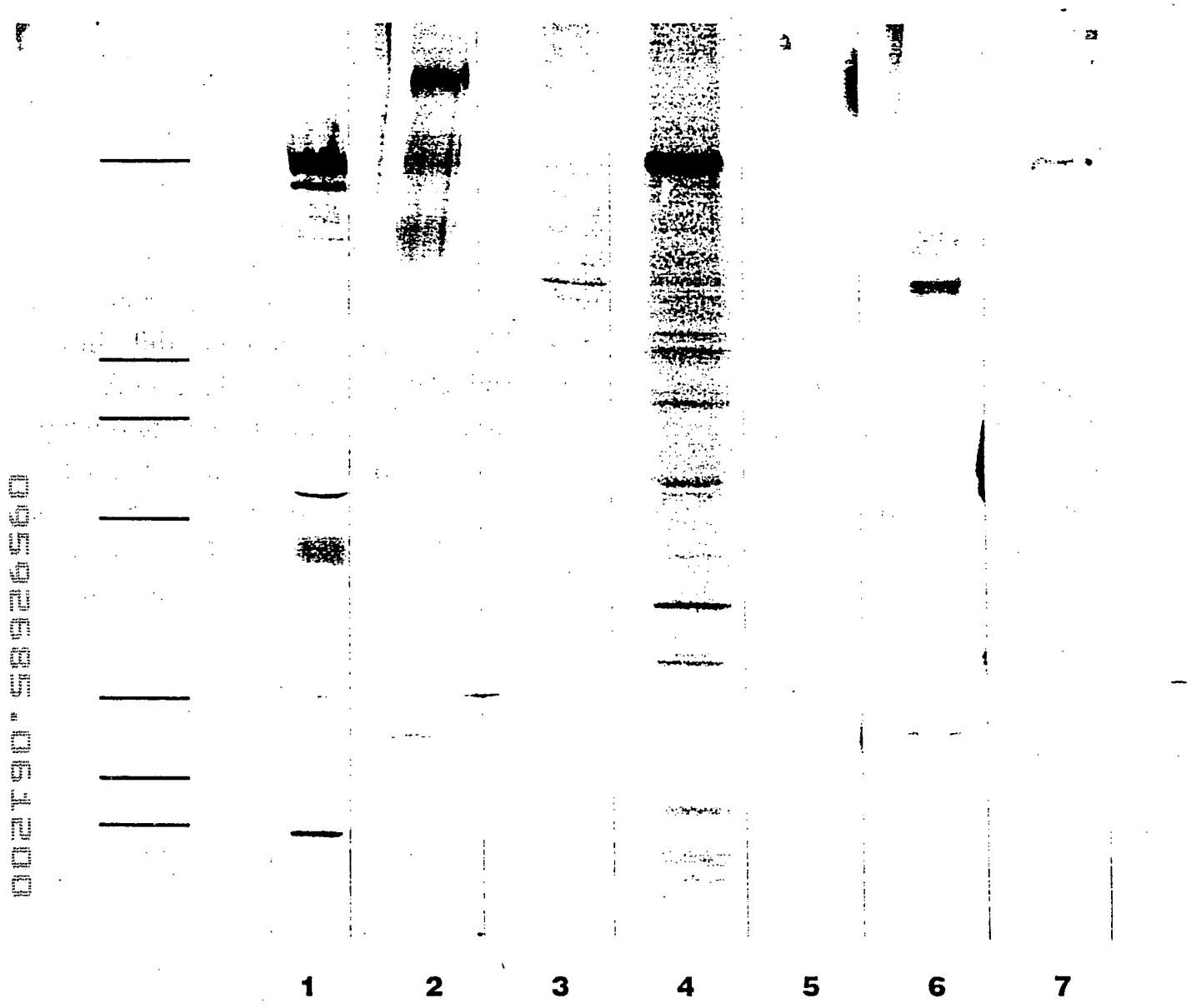

FIG. 13